

SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd

<120> Akt2 interacting protein

<130> Y0363-PCT

<150> JP2002-354155

<151> 2002-12-05

<150> JP2003-206952

<151> 2003-08-08

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 1722

<212> DNA

<213> Mus sp.

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<221> CDS

<222> (1).. (1719)

<223> Inventor: Endo, Yuki; Endoh, Hideki; Ueda, Yoshitaka; Kato, Miyuki;
Inabe, Kazunori

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atg gca gct gtg ccg ccc ctg cgg gac cgc ttg agc ttc ttg cat agg 48
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ctc ccc atc ctg ttg aag ggg acc tca gat gat agc atc cca tgt cca 96

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Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Ser Ile Pro Cys Pro
 20 25 30

ggc tac ctg ttt gaa gag atc gcc aag att tcc cac gag tca cta ggc 144
 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
 35 40 45

agc agc cag tgc ctg ctg gag tac ctc ctg aac cgt ctg gac agc agc 192
 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser
 50 55 60

tcc ggc cac gtg aag ctc aag gtg cta aag atc ttg ctt tac ctg tgt 240
 Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
 65 70 75 80

ggt cat ggc tct tcc tcc ttc ctc ctc atc ctc agg aga aac tct gct 288
 Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
 85 90 95

ctc atc caa gaa gcc acg gct ttc tca ggg cct cca gat cct ctt cac 336
 Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
 100 105 110

gga aat agc ttg tac cag aag gtg cgg gcg gct gcc cag gac ctg ggt 384
 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
 115 120 125

agc acc ctg ttc tca gat gcc gtg cca cag cct cca tcg cag cca cct 432
 Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro
 130 135 140

cag atc ccg cct ccc gca ggc atg ggc gcc cag gcc aga cct ctt agt 480
 Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
 145 150 155 160

gcc ctg caa ggc ttc ggc tac acg aag gag agc agc cgg aca ggc tcc 528

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Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
165 170 175

gca ggt gaa acc ttc ctc tcc acc atc cag agg gcc gca gag gta gtg 576
Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
180 185 190

gct aat gct gtg cgt cct gga cct gat aat cct tgt acc aag gga ccc 624
Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
195 200 205

ttg ccg tat ggt gat tcc tac cag cct gca gtg aca cct tca gct agc 672
Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
210 215 220

cac aca cat ccc aac cct ggg aat cta ctc cct ggg gcc atc ctg ggg 720
His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
225 230 235 240

gcc aga gct gtg aga cac cag ccc ggg cag gct ggg ggc ggc tgg gat 768
Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
245 250 255

gag ctg gac agc agt cct agt tcc cag aat tcc tcc tgc acc agc aac 816
Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
260 265 270

ctg agc agg gcc tog gac tcg ggc agt cgg tct ggc agt gac agc cac 864
Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His
275 280 285

tct ggc acc agc cgg gag cca ggc gac ctg gca gaa agg gct gag gcc 912
Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
290 295 300

acg ccc cca aat gac tgc cag caa gaa ctg aat cta gtg agg act gtg 960

Thr	Pro	Pro	Asn	Asp	Cys	Gln	Gln	Glu	Leu	Asn	Leu	Val	Arg	Thr	Val		
305					310					315					320		
aca	cag	ggg	cca	cgt	gtc	ttc	ctg	agc	cgt	gag	gag	acg	cag	cac	ttc		1008
Thr	Gln	Gly	Pro	Arg	Val	Phe	Leu	Ser	Arg	Glu	Glu	Thr	Gln	His	Phe		
				325					330					335			
atc	aaa	gag	tgt	ggc	ctg	ctc	aac	tgt	gag	gca	gtg	ctg	gag	ctg	ctc		1056
Ile	Lys	Glu	Cys	Gly	Leu	Leu	Asn	Cys	Glu	Ala	Val	Leu	Glu	Leu	Leu		
			340					345					350				
ctg	cgc	cag	ctg	gtc	ggg	acc	agt	gag	tgc	gag	cag	atg	agg	gcg	ctg		1104
Leu	Arg	Gln	Leu	Val	Gly	Thr	Ser	Glu	Cys	Glu	Gln	Met	Arg	Ala	Leu		
			355				360					365					
tgt	gcc	atc	gcg	tcc	ttt	ggg	agt	gct	gac	ctc	ctg	cct	cag	gag	cac		1152
Cys	Ala	Ile	Ala	Ser	Phe	Gly	Ser	Ala	Asp	Leu	Leu	Pro	Gln	Glu	His		
	370					375				380							
gtc	ctc	ctc	ctg	tgc	cga	cag	cag	ctg	cag	gaa	ctt	ggc	gcg	ggc	agc		1200
Val	Leu	Leu	Leu	Cys	Arg	Gln	Gln	Leu	Gln	Glu	Leu	Gly	Ala	Gly	Ser		
385				390					395					400			
cct	gga	cct	gtg	acc	aac	aaa	gcc	acc	aag	atc	ctg	aga	cat	ttt	gaa		1248
Pro	Gly	Pro	Val	Thr	Asn	Lys	Ala	Thr	Lys	Ile	Leu	Arg	His	Phe	Glu		
				405					410					415			
gcc	tcc	tgt	gga	caa	cag	ctc	cct	acc	cta	agg	ctc	tgt	gcc	cag	ccc		1296
Ala	Ser	Cys	Gly	Gln	Gln	Leu	Pro	Thr	Leu	Arg	Leu	Cys	Ala	Gln	Pro		
			420					425					430				
aac	tct	gca	gct	gcc	cct	gtg	ggc	cca	gct	gac	ctg	ctg	acc	agc	ccc		1344
Asn	Ser	Ala	Ala	Ala	Pro	Val	Gly	Pro	Ala	Asp	Leu	Leu	Thr	Ser	Pro		
			435				440					445					
gtg	cct	gcc	cct	ggg	agc	cag	gtc	tgc	ctc	cag	cct	ctc	agc	tcc	gcc		1392

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Val	Pro	Ala	Pro	Gly	Ser	Gln	Val	Cys	Leu	Gln	Pro	Leu	Ser	Ser	Ala	
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aca gtg gta ccc agg agt cct gtg ctc ttt cca tcc ccc aat acc tta																1440
Thr	Val	Val	Pro	Arg	Ser	Pro	Val	Leu	Phe	Pro	Ser	Pro	Asn	Thr	Leu	
465					470					475					480	
cct ccg tct gct ctg gag gag ccc agc gag gtc cga acc caa ttg gtg																1488
Pro	Pro	Ser	Ala	Leu	Glu	Glu	Pro	Ser	Glu	Val	Arg	Thr	Gln	Leu	Val	
				485					490					495		
tgt tct agt gaa cag ggg aca gaa tct gag cag agg ctg gag aac aca																1536
Cys	Ser	Ser	Glu	Gln	Gly	Thr	Glu	Ser	Glu	Gln	Arg	Leu	Glu	Asn	Thr	
			500					505					510			
gac acc cca gag gat agc tcc agt ccg ctc ccg tgg agt ccc aac tct																1584
Asp	Thr	Pro	Glu	Asp	Ser	Ser	Ser	Pro	Leu	Pro	Trp	Ser	Pro	Asn	Ser	
			515					520					525			
ttg ttt gct ggc atg gag ctg gtg gct tgc ccc cgc ctg cct tgc cac																1632
Leu	Phe	Ala	Gly	Met	Glu	Leu	Val	Ala	Cys	Pro	Arg	Leu	Pro	Cys	His	
		530					535				540					
agc tcg cag gac ctc cag aca gat tta cag aag gtg acc aca gaa gct																1680
Ser	Ser	Gln	Asp	Leu	Gln	Thr	Asp	Leu	Gln	Lys	Val	Thr	Thr	Glu	Ala	
545				550						555					560	
ccg gtt tca gag cca tca gct ttt gca ttt tta aac atg tga																1722
Pro	Val	Ser	Glu	Pro	Ser	Ala	Phe	Ala	Phe	Leu	Asn	Met				
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 <212> PRT
 <213> Mus sp.

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<400> 2

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20 25 30

Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
35 40 45

Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser
50 55 60

Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
65 70 75 80

Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
85 90 95

Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
100 105 110

Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
115 120 125

Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro

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130

135

140

Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
145 150 155 160

Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
165 170 175

Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
180 185 190

Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
195 200 205

Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
210 215 220

His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
225 230 235 240

Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
245 250 255

Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
260 265 270

Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His

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275

280

285

Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
290 295 300

Thr Pro Pro Asn Asp Cys Gln Gln Glu Leu Asn Leu Val Arg Thr Val
305 310 315 320

Thr Gln Gly Pro Arg Val Phe Leu Ser Arg Glu Glu Thr Gln His Phe
325 330 335

Ile Lys Glu Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Glu Leu Leu
340 345 350

Leu Arg Gln Leu Val Gly Thr Ser Glu Cys Glu Gln Met Arg Ala Leu
355 360 365

Cys Ala Ile Ala Ser Phe Gly Ser Ala Asp Leu Leu Pro Gln Glu His
370 375 380

Val Leu Leu Leu Cys Arg Gln Gln Leu Gln Glu Leu Gly Ala Gly Ser
385 390 395 400

Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe Glu
405 410 415

Ala Ser Cys Gly Gln Gln Leu Pro Thr Leu Arg Leu Cys Ala Gln Pro

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420

425

430

Asn Ser Ala Ala Ala Pro Val Gly Pro Ala Asp Leu Leu Thr Ser Pro
435 440 445

Val Pro Ala Pro Gly Ser Gln Val Cys Leu Gln Pro Leu Ser Ser Ala
450 455 460

Thr Val Val Pro Arg Ser Pro Val Leu Phe Pro Ser Pro Asn Thr Leu
465 470 475 480

Pro Pro Ser Ala Leu Glu Glu Pro Ser Glu Val Arg Thr Gln Leu Val
485 490 495

Cys Ser Ser Glu Gln Gly Thr Glu Ser Glu Gln Arg Leu Glu Asn Thr
500 505 510

Asp Thr Pro Glu Asp Ser Ser Ser Pro Leu Pro Trp Ser Pro Asn Ser
515 520 525

Leu Phe Ala Gly Met Glu Leu Val Ala Cys Pro Arg Leu Pro Cys His
530 535 540

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545 550 555 560

Pro Val Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn Met

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565

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<211> 1782
<212> DNA
<213> Homo sapiens

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<222> (1)..(1782)
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ctc ccg att ctc ctg aag ggg acg tcc gat gat gat gtc ccg tgt ccg 96
Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Asp Val Pro Cys Pro
20 25 30

ggc tac ctg ttt gaa gag att gct aaa atc tcc cac gag tct ccg ggc 144
Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Pro Gly
35 40 45

agc agc cag tgc ctg ctg gag tac ctc ctg agc cgc ctg cac agc agc 192
Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Ser Arg Leu His Ser Ser
50 55 60

tcc ggc cac ggg aag ctc aag gtg ctg aag atc ctg ctc tat ctg tgc 240
Ser Gly His Gly Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
65 70 75 80

agc cac ggc tcc tcc ttc ttc ctg ctc atc ctc aaa cgc aac tct gcc 288
Ser His Gly Ser Ser Phe Phe Leu Leu Ile Leu Lys Arg Asn Ser Ala

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85	90	95	
ttc atc cag gaa gct gca gct ttt gca ggg ccc cca gat cct ctg cac			336
Phe Ile Gln Glu Ala Ala Ala Phe Ala Gly Pro Pro Asp Pro Leu His			
100	105	110	
ggg aac agc ttg tac cag aag gtt cgc gcg gcc gcg cag gac ttg ggg			384
Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly			
115	120	125	
agc acc ctg ttc tcg gac acc gtg ttg ccg ctg gct ccc tcc cag cct			432
Ser Thr Leu Phe Ser Asp Thr Val Leu Pro Leu Ala Pro Ser Gln Pro			
130	135	140	
ctg ggg acc ccg cct gcc aca ggc atg ggc tcc cag gcc agg ccg cac			480
Leu Gly Thr Pro Pro Ala Thr Gly Met Gly Ser Gln Ala Arg Pro His			
145	150	155	160
agc acc ctc cag ggt ttc ggc tac agc aag gaa cac ggc cgc acg ggc			528
Ser Thr Leu Gln Gly Phe Gly Tyr Ser Lys Glu His Gly Arg Thr Gly			
165	170	175	
tcg gca ggc gaa gcc ttc ctc tcc acc atc cag aag gcc gca gag gtg			576
Ser Ala Gly Glu Ala Phe Leu Ser Thr Ile Gln Lys Ala Ala Glu Val			
180	185	190	
gtg gcc agc gcc atg cgc ccc ggg ccc gag agt ccc agt acc cgg agg			624
Val Ala Ser Ala Met Arg Pro Gly Pro Glu Ser Pro Ser Thr Arg Arg			
195	200	205	
ctc ctg ccg cgg ggt gac acc tac cag cct gcc atg atg cct tca gcc			672
Leu Leu Pro Arg Gly Asp Thr Tyr Gln Pro Ala Met Met Pro Ser Ala			
210	215	220	
agc cac ggt ccc cca acc ctg ggg aac cta ctc ccc ggg gcc att cca			720
Ser His Gly Pro Pro Thr Leu Gly Asn Leu Leu Pro Gly Ala Ile Pro			

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225	230	235	240	
ggt ccc cga gct gtg agg cat cag cct ggg cag gcc gga ggg ggc tgg				768
Gly Pro Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp				
	245	250	255	
gat gag ctg gac agc ggc ccc agc tct cag aat tcc tcc cag aac agc				816
Asp Glu Leu Asp Ser Gly Pro Ser Ser Gln Asn Ser Ser Gln Asn Ser				
	260	265	270	
gac ctg agc agg gtc tcg gac tcg ggc agt cat tcc ggc agc gac agc				864
Asp Leu Ser Arg Val Ser Asp Ser Gly Ser His Ser Gly Ser Asp Ser				
	275	280	285	
cat tca ggg gcc agc cgg gag ccg ggt gac ctg gca gaa agg gtc gag				912
His Ser Gly Ala Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Val Glu				
	290	295	300	
gtg gtg gcc ctg agt gac tgt cag cag gag ttg agc ttg gtg agg act				960
Val Val Ala Leu Ser Asp Cys Gln Gln Glu Leu Ser Leu Val Arg Thr				
305	310	315	320	
gtg act cgg gga cca cgc gcc ttc ctg agc cgc gag gag gca cag cac				1008
Val Thr Arg Gly Pro Arg Ala Phe Leu Ser Arg Glu Glu Ala Gln His				
	325	330	335	
ttc atc aaa gcg tgt gga ctg ctc aac tgt gag gcc gtg ctg cag ctg				1056
Phe Ile Lys Ala Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Gln Leu				
	340	345	350	
ctg acc tgc cac ctg cgt ggg acc agt gaa tgc acg cag ctg agg gcg				1104
Leu Thr Cys His Leu Arg Gly Thr Ser Glu Cys Thr Gln Leu Arg Ala				
	355	360	365	
ctg tgt gcc atc gcc tcc ctg ggg agc agc gac ctc ctc ccc cag gag				1152
Leu Cys Ala Ile Ala Ser Leu Gly Ser Ser Asp Leu Leu Pro Gln Glu				

370	375	380	
cac atc ctc ctc cgc acc cgg ccg tgg ctg cag gag ctc agc atg ggc			1200
His Ile Leu Leu Arg Thr Arg Pro Trp Leu Gln Glu Leu Ser Met Gly			
385	390	395	400
agc ccg gga cct gtg acc aac aag gcc acc aag atc ctg agg cac ttt			1248
Ser Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe			
	405	410	415
gag gcc tcc tgt ggg cag ctg tcc cct gcc cgg ggc acc tca gct gag			1296
Glu Ala Ser Cys Gly Gln Leu Ser Pro Ala Arg Gly Thr Ser Ala Glu			
	420	425	430
cct ggc ccc aca gcc gcc ctc cca ggc cca tct gac ctg ctg acc gac			1344
Pro Gly Pro Thr Ala Ala Leu Pro Gly Pro Ser Asp Leu Leu Thr Asp			
	435	440	445
gct gtg cct ctc cct ggg agc cag gtc ttc ctg cag cct ctg agt tca			1392
Ala Val Pro Leu Pro Gly Ser Gln Val Phe Leu Gln Pro Leu Ser Ser			
	450	455	460
acc ccg gtc tcg tcc cgg agc cct gct ccc tca tct ggg atg ccg tcc			1440
Thr Pro Val Ser Ser Arg Ser Pro Ala Pro Ser Ser Gly Met Pro Ser			
	465	470	475
agc cct gtg ccc acc cca ccc cca gat gcc tcc ccc att cca gcc ccc			1488
Ser Pro Val Pro Thr Pro Pro Pro Asp Ala Ser Pro Ile Pro Ala Pro			
	485	490	495
gga gac ccc agc gag gcc gag gcc aga ctg gca gaa agc agg cgg tgg			1536
Gly Asp Pro Ser Glu Ala Glu Ala Arg Leu Ala Glu Ser Arg Arg Trp			
	500	505	510
aga cct gaa cgg atc ccg ggg ggc acg gac agc cca aag aga ggc ccc			1584
Arg Pro Glu Arg Ile Pro Gly Gly Thr Asp Ser Pro Lys Arg Gly Pro			

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520

525

agc agc tgt gcg tgg agc cgc gac tcc ttg ttt gct ggc atg gag ctg 1632
Ser Ser Cys Ala Trp Ser Arg Asp Ser Leu Phe Ala Gly Met Glu Leu
530 535 540

gtg gcc tgt ccc cgc ctg gtg ggg gct ggg gct gct gcg gga gag tcc 1680
Val Ala Cys Pro Arg Leu Val Gly Ala Gly Ala Ala Ala Gly Glu Ser
545 550 555 560

tgt cct gat gct ccc cgc gcc ccc caa aca tcg tcc cag agg aca gca 1728
Cys Pro Asp Ala Pro Arg Ala Pro Gln Thr Ser Ser Gln Arg Thr Ala
565 570 575

gcc aaa gag cct cct ggc tca gag ccg tca gct ttc gcg ttc ctg aac 1776
Ala Lys Glu Pro Pro Gly Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn
580 585 590

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gcc tga                                     1782
Ala
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<210> 4

<211> 593.

<212> PRT

<213> Homo sapiens

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Met Ala Ala Ala Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
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Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Asp Val Pro Cys Pro
20 25 30

Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Pro Gly
 35 40 45

Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Ser Arg Leu His Ser Ser
 50 55 60

Ser Gly His Gly Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
 65 70 75 80

Ser His Gly Ser Ser Phe Phe Leu Leu Ile Leu Lys Arg Asn Ser Ala
 85 90 95

Phe Ile Gln Glu Ala Ala Ala Phe Ala Gly Pro Pro Asp Pro Leu His
 100 105 110

Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
 115 120 125

Ser Thr Leu Phe Ser Asp Thr Val Leu Pro Leu Ala Pro Ser Gln Pro
 130 135 140

Leu Gly Thr Pro Pro Ala Thr Gly Met Gly Ser Gln Ala Arg Pro His
 145 150 155 160

Ser Thr Leu Gln Gly Phe Gly Tyr Ser Lys Glu His Gly Arg Thr Gly
 165 170 175

Ser Ala Gly Glu Ala Phe Leu Ser Thr Ile Gln Lys Ala Ala Glu Val
 180 185 190

Val Ala Ser Ala Met Arg Pro Gly Pro Glu Ser Pro Ser Thr Arg Arg
 195 200 205

Leu Leu Pro Arg Gly Asp Thr Tyr Gln Pro Ala Met Met Pro Ser Ala
 210 215 220

Ser His Gly Pro Pro Thr Leu Gly Asn Leu Leu Pro Gly Ala Ile Pro
 225 230 235 240

Gly Pro Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp
 245 250 255

Asp Glu Leu Asp Ser Gly Pro Ser Ser Gln Asn Ser Ser Gln Asn Ser
 260 265 270

Asp Leu Ser Arg Val Ser Asp Ser Gly Ser His Ser Gly Ser Asp Ser
 275 280 285

His Ser Gly Ala Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Val Glu
 290 295 300

Val Val Ala Leu Ser Asp Cys Gln Gln Glu Leu Ser Leu Val Arg Thr
 305 310 315 320

Val Thr Arg Gly Pro Arg Ala Phe Leu Ser Arg Glu Glu Ala Gln His
325 330 - 335

Phe Ile Lys Ala Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Gln Leu
340 345 350

Leu Thr Cys His Leu Arg Gly Thr Ser Glu Cys Thr Gln Leu Arg Ala
355 360 365

Leu Cys Ala Ile Ala Ser Leu Gly Ser Ser Asp Leu Leu Pro Gln Glu
370 375 380

His Ile Leu Leu Arg Thr Arg Pro Trp Leu Gln Glu Leu Ser Met Gly
385 390 395 400

Ser Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe
405 410 415

Glu Ala Ser Cys Gly Gln Leu Ser Pro Ala Arg Gly Thr Ser Ala Glu
420 425 430

Pro Gly Pro Thr Ala Ala Leu Pro Gly Pro Ser Asp Leu Leu Thr Asp
435 440 445

Ala Val Pro Leu Pro Gly Ser Gln Val Phe Leu Gln Pro Leu Ser Ser
450 455 460

Thr Pro Val Ser Ser Arg Ser Pro Ala Pro Ser Ser Gly Met Pro Ser
 465 470 475 480

Ser Pro Val Pro Thr Pro Pro Pro Asp Ala Ser Pro Ile Pro Ala Pro
 485 490 495

Gly Asp Pro Ser Glu Ala Glu Ala Arg Leu Ala Glu Ser Arg Arg Trp
 500 505 510

Arg Pro Glu Arg Ile Pro Gly Gly Thr Asp Ser Pro Lys Arg Gly Pro
 515 520 525

Ser Ser Cys Ala Trp Ser Arg Asp Ser Leu Phe Ala Gly Met Glu Leu
 530 535 540

Val Ala Cys Pro Arg Leu Val Gly Ala Gly Ala Ala Ala Gly Glu Ser
 545 550 555 560

Cys Pro Asp Ala Pro Arg Ala Pro Gln Thr Ser Ser Gln Arg Thr Ala
 565 570 575

Ala Lys Glu Pro Pro Gly Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn
 580 585 590

Ala

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<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

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cgtaccacgc tgccaccatg aatgagg

27

<210> 6
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<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

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gcagcgagcg tgcgtcctct gcgtggg

27

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<211> 61
<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

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agagagtagt aacaaaggtc aaagacagtt gactgtatcg atgaatgagg tgtctgtcat 60

c 61

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<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence: an artificially
synthesized primer sequence

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tggagacttg accaaacctc tggcgaagaa gtccaaagct tcactcgcgg atgctggc 58

<210> 9
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<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence: the sequence of 5183th(5') to
5162th(3') bases in Cloning vector pACT2 (GenBank U29899)

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cgcgtttgga atcactacag gg 22

<210> 10
<211> 24
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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 10

cagttgagca ggccacactc ttg

24

<210> 11

<211> 20

<212> DNA

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 11

taatacgact cactataggg

20

<210> 12

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 12

atggcagctg tgccgccc

18

<210> 13
<211> 21
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 13
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21

<210> 14
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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 14
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22

<210> 15
<211> 17
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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 15

caggcactgg ctgctgc

17

<210> 16

<211> 20

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 16

aaagtggaga ttgttgccat

20

<210> 17

<211> 19

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 17

ttgactgtgc cgttgaatt

19

<210> 18

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<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially

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<400> 18

atggctgccg cgccgcc

17

<210> 19

<211> 20

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 19

ggcggttcagg aacgcgaaag

20

<210> 20

<211> 18

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 20

gactgtgact cggggacc

18

<210> 21

<211> 21

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<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 21

gatccccggg tatogcatcc a

21

<210> 22

<211> 21

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 22

agcttggatg cgataccgg g

21

<210> 23

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<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 23

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19

<210> 24

<211> 39
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synthesized primer sequence

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39

<210> 25
<211> 38
<212> DNA
<213> Artificial

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 25
tcgagaccct ctgcgaacga tgaagttctt ggcottcc

38

<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 26
gggactacaa ggacgatgac gataagtagc

30

<210> 27

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 27

ggcgcgtact tatcgtcacg gtccttgtag tcccgc

36